Phylogeography of Two Species of Marine Sculpins

Lauren Bailey[1], Thaddaeus Buser[1,2], and J. Andrés López[1,2]

[1] School of Fisheries and Ocean Sciences; [2] University of Alaska Museum; University of Alaska Fairbanks

OBJECTIVES

- Describe the modern population structure of the tidepool sculpin (*Oligocottus maculosus*) and the sharpnose sculpin (*Clinocottus acuticeps*) in the context of their respective geographic distributions.
- Estimate the ways in which these species have been influenced by historic changes in climate and sea level.

INTRODUCTION

- Phylogeographic patterns among marine species may result from migration, selection, genetic drift, mutation and demographic history (Hickerson and Ross, 2001).
- The effects of Pleistocene glaciations on the populations of marine intertidal species in the North Eastern Pacific are not well understood (Hisckerson and Ross, 2001).
- The tidepool sculpin (*Oligocottus maculosus*) and sharpnose sculpin (*Clinocottus acuticeps*) are two species of common, intertidal fishes that inhabit the North American Pacific Coast from California to the Aleutian Islands (Fig. 1).
- Understanding the modern population structure of these species may give us clues as to the effect of historical changes in climate and sea level on intertidal species.

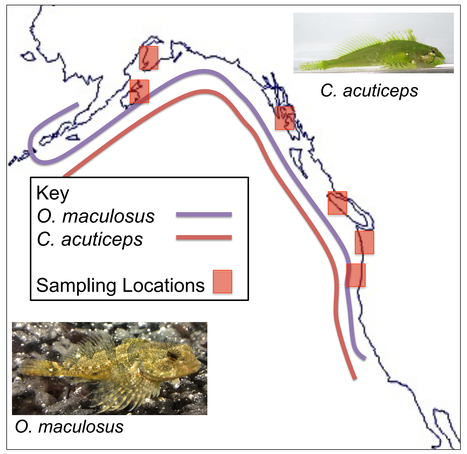

Figure 1: Range and sampling locations of *C. acuticeps* and *O. maculosus.*

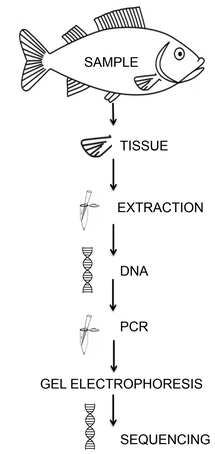

Figure 2: Tissue to sequence flowchart.

METHODS

1. DNA Extraction
- Tissues from *C. acuticeps* and *O. maculosus* were assembled from across the range of each species (Fig. 1)
- Qiagen Dneasy Extraction Kit using manufacturer's protocols (Fig 2).

2. Polymerase Chain Reaction (PCR)
- Two Genes
  -Mitochondrial (COI)
  -Nuclear (55305E1)
- 78 samples of *O. maculosus*
- 30 samples of *C. acuticeps*

3. Gel Electrophoresis
- Visual verification of amplification results (Fig 2).

4. Sequencing
- PCR Products were used in automated DNA sequencing
- University of Washington High-Throughput Genomics Unit
- Sequences visually checked for quality, edited, and assembled into contigs using CodonCode

5. Haplotype Network Construction
- Sequences were aligned using ClustalW
- Haplotype networks were constructed from alignments using TCS1.21 (Posada and Crandall 2000)

RESULTS AND CONCLUSION

RESULTS

- There appears to be very little correlation between collection location and haplotype (Fig 4-7).
- There is differential variation between the two species as well as between the two molecular loci.
- In *O. maculosus*, nuclear intron 55305E1 contains an insertion/deletion that accounts for the majority of the differentiation between haplotypes.
- The nuclear intron, EPIC Locus 55305E1, shows greater haplotype diversity than the mitochondrial gene, COI in both species, but especially in *C. acuticeps* (Fig 4-7

HAPLOTYPE NETWORKS

Size of bubble indicates frequency of haplotype, steps in network indicate single nucleotide mutations.

O. maculosus

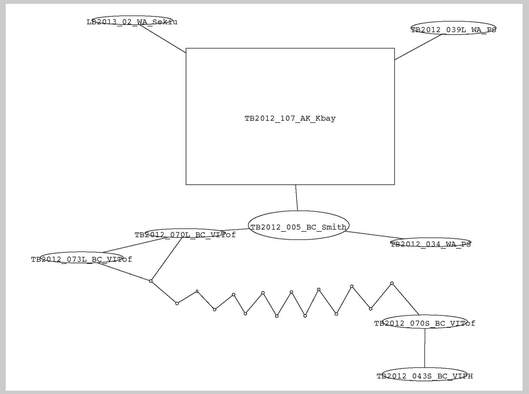

Figure 4: 55305E1 haplotype network.

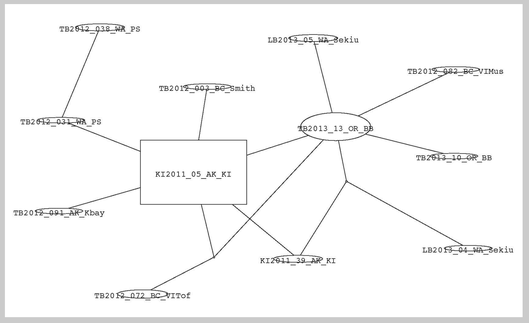

Figure 5: COI haplotype network.

C. acuticeps

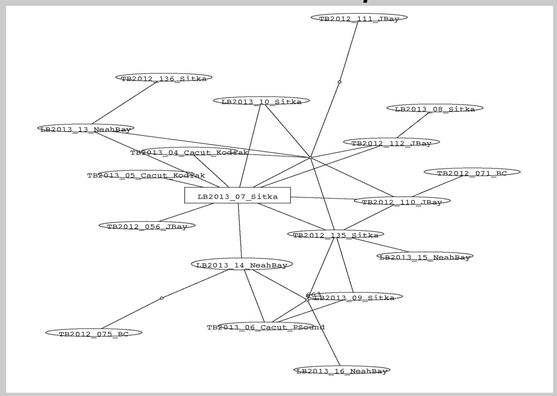

Figure 6: 55305E1 haplotype network.

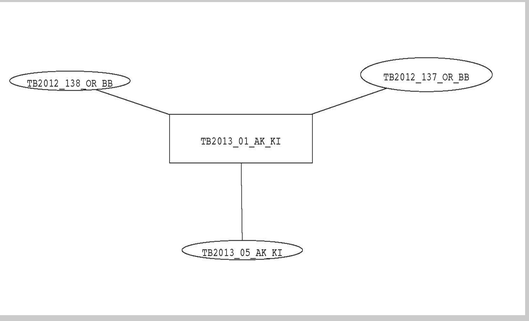

Figure 7: COI haplotype network.

CONCLUSIONS

- The lack of geography-based population structure could be explained in part by:
  - a) A high degree of gene flow among populations.
  - b) A very recent and rapid colonization of the present range of each species.
  - c) A combination of the above factors.
- Future work should include additional non-coding DNA regions such as the highly variable mitochondrial control region.

ACKNOWLEDGMENTS

Funding from Undergraduate Research and Scholarly Activity (URSA) Spring Project Award.

REFERENCES

- Clement M, D. Posada, and K. Crandall. 2000. TCS: a computer program to estimate gene genealogies. Molecular Ecology 9(10): 1657-1660.
- Hickerson, M. and J. Ross. 2001. Post-glacial population history and genetic structure of the northern clingfish (*Gobbiesox maeandricus*), revealed from mtDNA analysis. Marine Biology. 138. 407-419.
- Wares, J. 2002. Community genetics in the Northwestern Atlantic intertidal. Molecular Ecology. 11. 1131-1144.
- Yokoyama, R., V. Sideleva, S. Shedko and A. Goto. 2008. Broad-scale phylogeography of the Palearctic freshwater fish *Cottus poecilopus*. Molecular Phylogenetics and Evolution. 48. 1244-1251.